What is claimed is:

1. A method for the production of a soybean plant having an *rhg*1 SCN resistant allele comprising:

(A) crossing a first soybean plant having an *rhg*1 SCN resistant allele with a second soybean plant having an *rhg*1 SCN sensitive allele to produce a segregating population;

(B) screening said segregating population for a member having an *rhg*1 SCN resistant allele with a first nucleic acid molecule capable of specifically hybridizing to linkage group G, wherein said first nucleic acid molecule specifically hybridizes to a second nucleic acid molecule that is linked to said *rhg*1 SCN resistant allele; and,

(C) selecting said member for further crossing and selection.

2. The method for the production of a soybean plant according to claim 1, wherein said first nucleic acid molecule is capable of specifically hybridizing to said second nucleic acid molecule having the nucleic acid sequence of SEQ ID NO: 2, 3, complements thereof, or fragments thereof having at least 15 nucleotides.

3. The method for the production of a soybean plant according to claim 1, wherein said first nucleic acid molecule is capable of specifically hybridizing to said second nucleic acid molecule having the nucleic acid sequence of SEQ ID NO: 5 or 6, complements thereof, or fragments thereof having at least 15 nucleotides.

4. The method for the production of a soybean plant according to claim 1, wherein said first nucleic acid molecule is a nucleic acid marker capable of detecting *rhg*1 haplotype 2 or 4.

5. The method for the production of a soybean plant according to claim 1, wherein said first nucleic acid molecule is capable of specifically hybridizing to a nucleic acid molecule having a sequence that is present on linkage group G within 100kb of said *rhg*1 SCN sensitive allele.

6. The method for the production of a soybean plant according to claim 5, wherein said first nucleic acid molecule is capable of specifically hybridizing to a nucleic acid molecule having a

sequence that is present on linkage group G and located within 50kb of said *rhg*1 SCN sensitive allele.

7. The method for the production of a soybean plant according to claim 6, wherein said first nucleic acid molecule is capable of specifically hybridizing to a nucleic acid molecule having a sequence that is present on linkage group G and located within 25kb of said *rhg*1 SCN sensitive allele.

8. The method for the production of a soybean plant according to claim 7, wherein said *rhg*1 SCN sensitive allele is also present in soybean line A3244.

9. The method for the production of a soybean plant according to claim 1, wherein said first soybean plant having an *rhg*1 SCN resistant allele is selected from the soybean maturity group consisting of 000, 00, 0, I, II, III, IV, and V.

10. The method for the production of a soybean plant according to claim 1, wherein said first soybean plant having an *rhg*1 SCN resistant allele is selected from the soybean maturity group consisting of VI, VII, VIII, IX, and X.

11. A method of investigating an *rhg*1 haplotype of a soybean plant comprising:

(A) isolating nucleic acid molecules from said soybean plant;

(B) determining the nucleic acid sequence of an *rhg*1 allele or part thereof; and,

(C) comparing the nucleic acid sequence of said *rhg*1 allele or part thereof to a reference nucleic acid sequence.

12. The method of investigating an *rhg*1 haplotype of a soybean plant according to claim 11, wherein said determining of said nucleic acid sequence of said *rhg*1 allele or part thereof is a determination of a single nucleotide.

13. The method of investigating an *rhg*1 haplotype of a soybean plant according to claim 11, wherein said determining of said nucleic acid sequence of said *rhg*1 allele or part thereof is a determination of the nucleic acid sequence of an exon of *rhg*1.

14. The method of investigating an *rhg*1 haplotype of a soybean plant according to claim 13, wherein said exon is exon 1 of *rhg*1 *v.1*.

15. The method of investigating an *rhg*1 haplotype of a soybean plant according to claim 13, wherein said exon is exon 3 of *rhg*1 *v.1*.

16 The method of investigating an *rhg*1 haplotype of a soybean plant according to claim 13, wherein said exon is exon 1 of *rhg*1 *v.2*.

17. The method of investigating an *rhg*1 haplotype of a soybean plant according to claim 13, wherein said exon is exon 2 of *rhg*1 *v.2*.

18. The method of investigating an *rhg*1 haplotype of a soybean plant according to claim 13, wherein said determination of said nucleic acid sequence of said *rhg*1 allele or part thereof is a determination of the nucleic acid sequence of a leucine rich repeat domain.

19. A method of introgressing SCN resistance or partial SCN resistance into a soybean plant comprising:

performing marker assisted selection of said soybean plant with a nucleic acid marker, wherein said nucleic acid marker specifically hybridizes with a nucleic acid molecule having a first nucleic acid sequence that is physically linked to a second nucleic acid sequence that is located on linkage group G of soybean A3244, wherein said second nucleic acid sequence is within 500 kb of a third nucleic acid sequence which is capable of specifically hybridizing with the nucleic acid sequence of SEQ ID NO: 5, 6, complements thereof, or fragments thereof having at least 15 nucleotides; and,

selecting said soybean plant based on said marker assisted selection.

20. The method of introgressing SCN resistance or partial SCN resistance into a soybean plant according to claim 19, wherein said introgression of said SCN resistance or partial resistance is carried out by backcrossing with a sensitive soybean recurrent parent.

21. The method of introgressing SCN resistance or partial SCN resistance into a soybean plant according to claim 19, wherein said introgression of said SCN resistance or partial resistance is carried out by backcrossing with an *Rhg*4 SCN resistance soybean recurrent parent.

22. The method of introgressing SCN resistance or partial SCN resistance into a soybean plant according to claim 19, wherein said introgression of said SCN resistance or partial resistance is carried out by backcrossing with an elite soybean recurrent parent.

23. The method of introgressing SCN resistance or partial SCN resistance into a soybean plant according to claim 19, wherein said nucleic acid marker is selected from the group consisting of SEQ ID NOs: 54-1096 and complements thereof.

24. The method of introgressing SCN resistance or partial SCN resistance into a soybean plant according to claim 19, wherein said nucleic acid marker is capable of detecting a single nucleotide polymorphism selected from the group of those set forth in table 2.

25. The method of introgressing SCN resistance or partial SCN resistance into a soybean plant according to claim 19, wherein said nucleic acid marker is capable of detecting a SSR selected from the group consisting of SEQ ID NOs: 54-1096 and complements thereof.

26. The method of introgressing SCN resistance or partial SCN resistance into a soybean plant according to claim 19, wherein said physically linked second nucleic acid sequence is within 100 kb of a nucleic sequence which is capable of specifically hybridizing with the nucleic acid sequence of SEQ ID NO: 5, or 6, complements thereof, or fragments thereof having at least 15 nucleotides.

27. The method of introgressing SCN resistance or partial SCN resistance into a soybean plant according to claim 26, wherein said physically linked second nucleic acid sequence is within 50 kb of a nucleic sequence which is capable of specifically hybridizing with the nucleic acid sequence of SEQ ID NO: 5 or 6, complements thereof, or fragments thereof having at least 15 nucleotides.

28. The method of introgressing SCN resistance or partial SCN resistance into a soybean plant according to claim 27, wherein said physically linked second nucleic acid sequence is within 25 kb of a nucleic sequence which is capable of specifically hybridizing with the nucleic acid sequence of SEQ ID NO: 5 or 6, complements thereof, or fragments thereof having at least 15 nucleotides.

29. A method for the production of a soybean plant having an *Rhg*4 SCN resistant allele comprising:

(A) crossing a first soybean plant having an *Rhg*4 SCN resistant allele with a second soybean plant having an *Rhg*4 SCN sensitive allele to produce a segregating population;

(B) screening the segregating population for a member having an *Rhg*4 SCN resistant allele with a first nucleic acid molecule capable of specifically hybridizing to linkage group A2, wherein said first nucleic acid molecule specifically hybridizes to a second nucleic acid molecule linked to said *Rhg*4 SCN resistant allele; and,

(C) selecting said member for further crossing and selection.

30. The method for the production of a soybean plant according to claim 29, wherein said first nucleic acid molecule is capable of specifically hybridizing to said second nucleic acid molecule having the nucleic acid sequence of SEQ ID NO: 4, complements thereof, or fragments thereof having at least 15 nucleotides.

31. The method for the production of a soybean plant according to claim 29, wherein said first nucleic acid molecule is capable of specifically hybridizing to said second nucleic acid molecule having the nucleic acid sequence of SEQ ID NO: 7, complements thereof, or fragments thereof having at least 15 nucleotides.

32. The method for the production of a soybean plant according to claim 29, wherein said nucleic acid molecule is a nucleic acid marker capable of detecting *Rhg*4 haplotype 3.

33. The method for the production of a soybean plant according to claim 29, wherein said first nucleic acid molecule is capable of specifically hybridizing to a nucleic acid molecule having a sequence that is present on linkage group A2 within 100kb of said *Rhg*4 SCN sensitive allele.

34. The method for the production of a soybean plant according to claim 33, wherein said first nucleic acid molecule is capable of specifically hybridizing to a nucleic acid molecule having a sequence that is present on linkage group A2 and located within 50kb of said *Rhg*4 SCN sensitive allele.

35. The method for the production of a soybean plant according to claim 34, wherein said first nucleic acid molecule is capable of specifically hybridizing to a nucleic acid molecule having a sequence that is present on linkage group A2 and located within 25kb of said *Rhg*4 SCN sensitive allele.

36. The method for the production of a soybean plant according to claim 35, wherein said *Rhg*4 SCN sensitive allele is also present in soybean line A3244.

37. The method for the production of a soybean plant according to claim 29, wherein said first soybean plant having an *Rhg*4 SCN resistant allele is selected from the soybean maturity group consisting of 000, 00, 0, I, II, III, IV, and V.

38. The method for the production of a soybean plant according to claim 29, wherein said first soybean plant having an *Rhg*4 SCN resistant allele is is selected from the soybean maturity group consisting of VI, VII, VIII, IX, and X.

39. A method of investigating an *Rhg*4 haplotype of a soybean plant comprising:

(A) isolating nucleic acid molecules from said soybean plant;

(B) determining the nucleic acid sequence of an *Rhg*4 allele or part thereof; and

(C) comparing the nucleic acid sequence of said *Rhg*4 allele or part thereof to a reference nucleic acid sequence.

40. The method of investigating an *Rhg*4 haplotype of a soybean plant according to claim 39, wherein said determining of said nucleic acid sequence of said *Rhg*4 allele or part thereof is a determination of a single nucleotide.

41. The method of investigating an *Rhg*4 haplotype of a soybean plant according to claim 39, wherein said determining of said nucleic acid sequence of said *Rhg*4 allele or part thereof is a determination of the nucleic acid sequence of an exon of *Rhg*4.

42. The method of investigating an *Rhg*4 haplotype of a soybean plant according to claim 41, wherein said exon is exon 1.

43. The method of investigating an *Rhg*4 haplotype of a soybean plant according to claim 41, wherein said exon is exon 2.

44. The method of investigating an *Rhg*4 haplotype of a soybean plant according to claim 41, wherein said determination of said nucleic acid sequence of said *Rhg*4 allele or part thereof is a determination of the nucleic acid sequence of a leucine rich repeat domain.

45. A method of introgressing SCN resistance or partial SCN resistance into a soybean plant comprising:

performing marker assisted selection of said soybean plant with a nucleic acid marker, wherein said nucleic acid marker specifically hybridizes with a nucleic acid molecule having a first nucleic acid sequence that is physically linked to a second nucleic acid sequence that is located on linkage group A2 of soybean A3244, wherein said second nucleic acid sequence is within 500 kb of a third nucleic acid sequence which specifically hybridizes with the nucleic acid sequence of SEQ ID NO: 7, complements thereof, or fragments thereof having at least 15 nucleotides; and,

selecting said soybean plant based on said marker assisted selection.

46. The method of introgressing SCN resistance or partial SCN resistance into a soybean plant according to claim 45, wherein said introgression of said SCN resistance or partial resistance is carried out by backcrossing with a sensitive soybean recurrent parent.

47. The method of introgressing SCN resistance or partial SCN resistance into a soybean plant according to claim 45, wherein said introgression of said SCN resistance or partial resistance is carried out by backcrossing with an *Rhg*1 SCN resistance soybean recurrent parent.

48. The method of introgressing SCN resistance or partial SCN resistance into a soybean plant according to claim 45, wherein said introgression of said SCN resistance or partial resistance is carried out by backcrossing with an elite soybean recurrent parent.

49. The method of introgressing SCN resistance or partial SCN resistance into a soybean plant according to claim 45, wherein said nucleic acid marker is selected from the group consisting of SEQ ID NOs: 54-1096 and complements thereof.

50. The method of introgressing SCN resistance or partial SCN resistance into a soybean plant according to claim 45, wherein said nucleic acid marker is capable of detecting a single nucleotide polymorphism selected from the group consisting of those set forth in table 4.

51. The method of introgressing SCN resistance or partial SCN resistance into a soybean plant according to claim 45, wherein said nucleic acid marker is capable of detecting a SSR selected from the group consisting of SEQ ID NOs: 54-1096 and complements thereof.

52. The method of introgressing SCN resistance or partial SCN resistance into a soybean plant according to claim 45, wherein said physically linked second nucleic acid sequence is within 100 kb of a nucleic sequence which specifically hybridizes with the nucleic acid sequence of SEQ ID NO: 7 or complement thereof.

53. The method of introgressing SCN resistance or partial SCN resistance into a soybean plant according to claim 45, wherein said physically linked second nucleic acid sequence is within 50 kb of a nucleic sequence which is capable of specifically hybridizing with the nucleic acid sequence of SEQ ID NO: 7, complements thereof, or fragments thereof having at least 15 nucleotides.

54. The method of introgressing SCN resistance or partial SCN resistance into a soybean plant according to claim 45, wherein said physically linked second nucleic acid sequence is within 25 kb of a nucleic sequence which is capable of specifically hybridizing with the nucleic acid sequence of SEQ ID NO: 7, complements thereof, or fragments thereof having at least 15 nucleotides.

55. A substantially purified nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 5, 6, 8-23, 28-43, complements thereof, and fragments of either.

56. A substantially purified first nucleic acid molecule with nucleic acid sequence which specifically hybridizes to a second nucleic acid molecule having a nucleic acid sequence selected from the group consisting of a complement of SEQ ID NOs: 5, 6, 8-23, 28-43.

57. A substantially purified nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 7, 44-47, and 50-53, complements thereof, and fragments of either.

58. A substantially purified first nucleic acid molecule with nucleic acid sequence which specifically hybridizes to a second nucleic acid molecule having a nucleic acid sequence selected from the group consisting of a complement of SEQ ID NOs: 50-53.

59. A substantially purified protein or fragment thereof comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 1097, 1098, and 1100-1115 and fragments thereof.

60. A substantially purified protein or fragment thereof comprising an amino acid sequence selected from the group consisting of SEQ ID NOs 1099, and 1116-1119 and fragments thereof.

61. A transformed plant having a nucleic acid molecule which comprises: (A) an exogenous promoter region which functions in a plant cell to cause the production of a mRNA molecule; (B) a structural nucleic acid molecule encoding a protein or fragment thereof comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 1097, 1100, 1098, 1101, 1102-1115; and (C) a 3' non-translated sequence that functions in the plant cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule.

62. The transformed plant according to claim 61, wherein said plant is soybean.

63. The transformed plant according to claim 62, wherein said plant is soybean is selected from the group consisting of PI548402 (Peking), PI200499, A2869, Jack, A2069, PI209332 (No:4), PI404166 (Krasnoaarmejkaja), PI404198 (Sun huan do), PI437654 (Er-hej-jan), PI438489 (Chiquita), PI507354 (Tokei 421), PI548655 (Forrest), PI548988 (Pickett), PI84751, PI437654, PI40792, Pyramid, Nathan, AG2201, A3469, AG3901, A3904, AG4301, AG4401, AG4501, AG4601, PION9492, PI88788, Dyer, Custer, Manokin, and Doles.

64. The transformed plant according to claim 61, wherein said promoter is an *rhg*1 promoter.

65. The transformed plant according to claim 61, wherein said promoter is an *Rhg*4 promoter.

66. A transformed plant having a nucleic acid molecule which comprises: (A) an exogenous promoter region which functions in a plant cell to cause the production of a mRNA molecule;

(B) a structural nucleic acid molecule encoding a protein or fragment thereof comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 1099, 1116-1119; and (C) a 3' non-translated sequence that functions in the plant cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule.

67. The transformed plant according to claim 66, wherein said plant is soybean.

68. The transformed plant according to claim 67, wherein said plant is soybean is selected from the group consisting of PI548402 (Peking), PI437654 (Er-hej-jan), PI438489 (Chiquita), PI507354 (Tokei 421), PI548655 (Forrest), PI548988 (Pickett), PI88788, PI404198 (Sun Huan Do), PI404166 (Krasnoaarmejkaja), Hartwig, Manokin, Doles, Dyer, and Custer.

69. The transformed plant according to claim 66, wherein said promoter is an *rhg*1 promoter.

70. The transformed plant according to claim 66, wherein said promoter is an *Rhg*4 promoter.

71. A transgenic seed having a nucleic acid molecule which comprises: (A) an exogenous promoter region which functions to cause the production of a mRNA molecule; (B) a structural nucleic acid molecule encoding a protein or fragment thereof comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 1097, 1100, 1098, 1101, 1102-1115; and (C) a 3' non-translated sequence that functions to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule.

72. A transgenic seed having a nucleic acid molecule which comprises: (A) an exogenous promoter region which functions to cause the production of a mRNA molecule; (B) a structural nucleic acid molecule encoding a protein or fragment thereof comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 1099, 1116-1119; and (C) a 3' non-translated sequence that functions to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule.